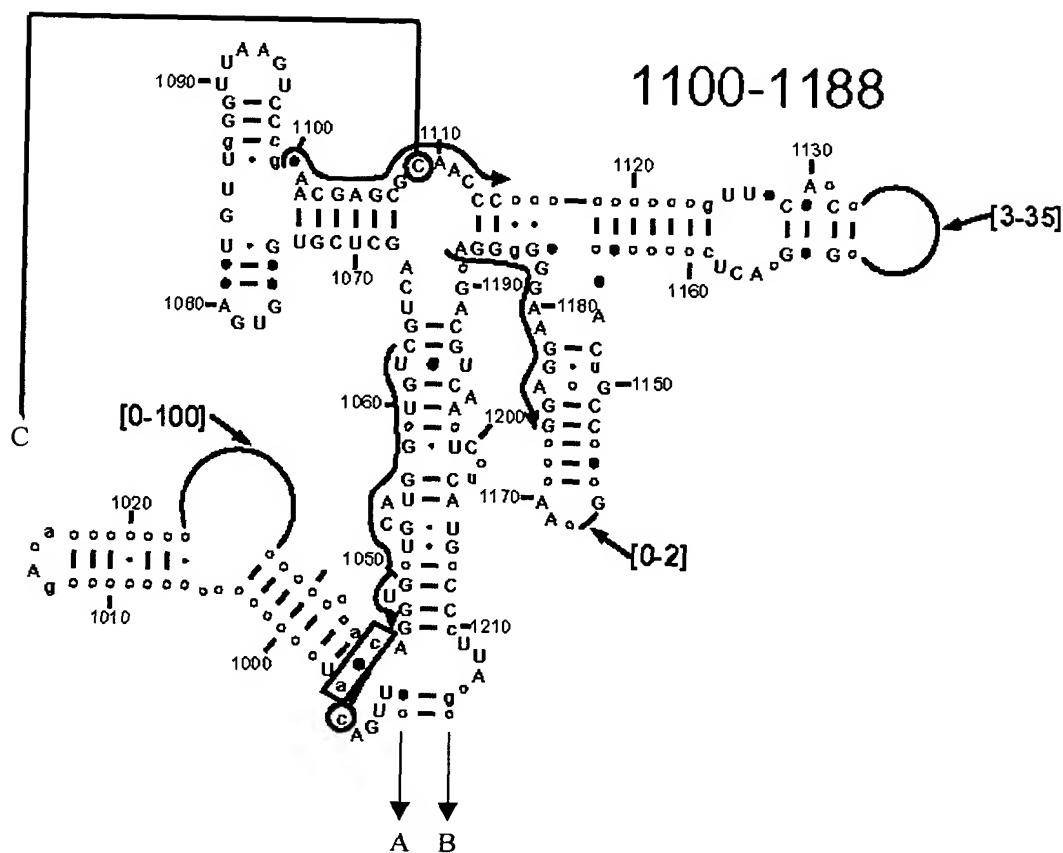


FIG. 1A-1



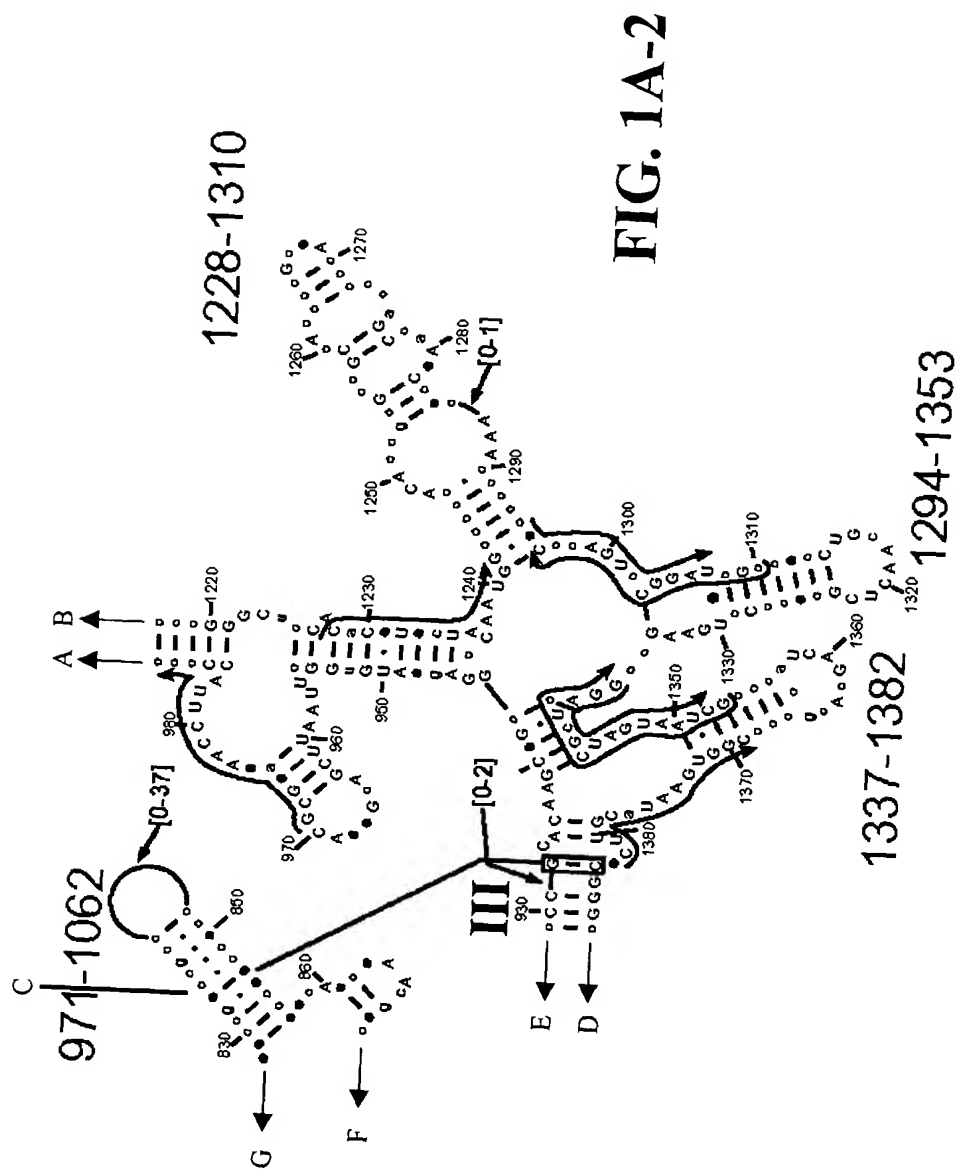


FIG. 1A-3

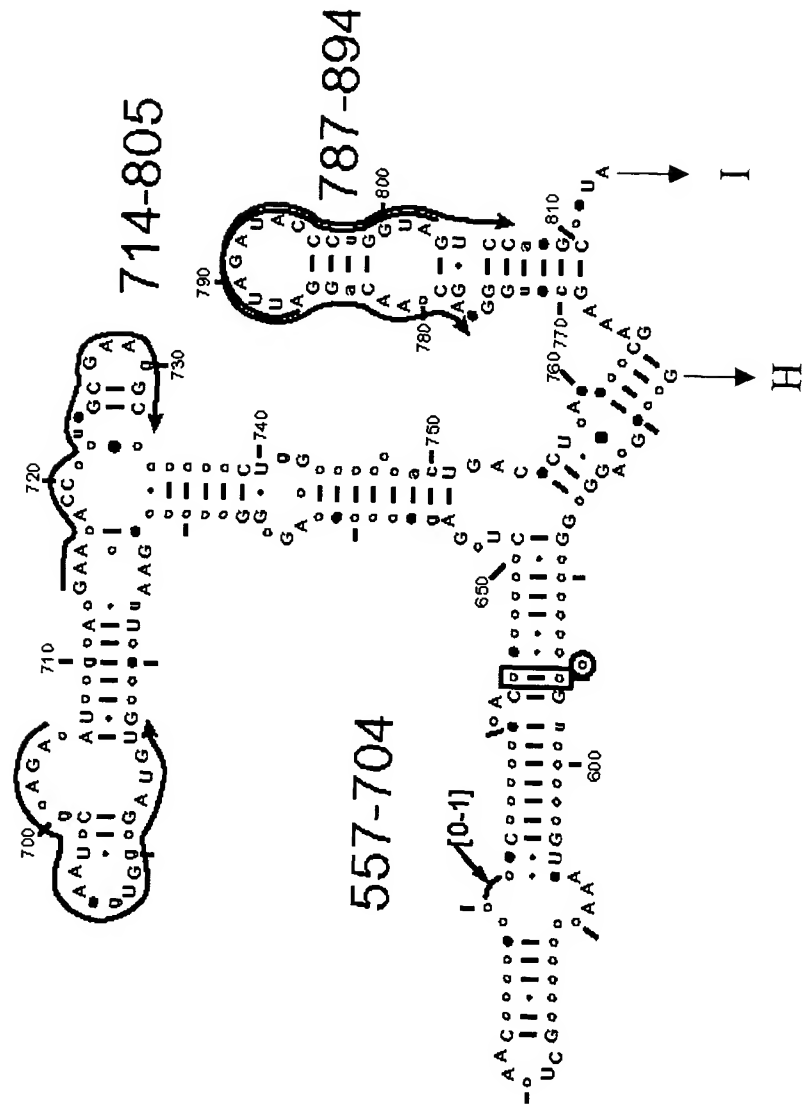
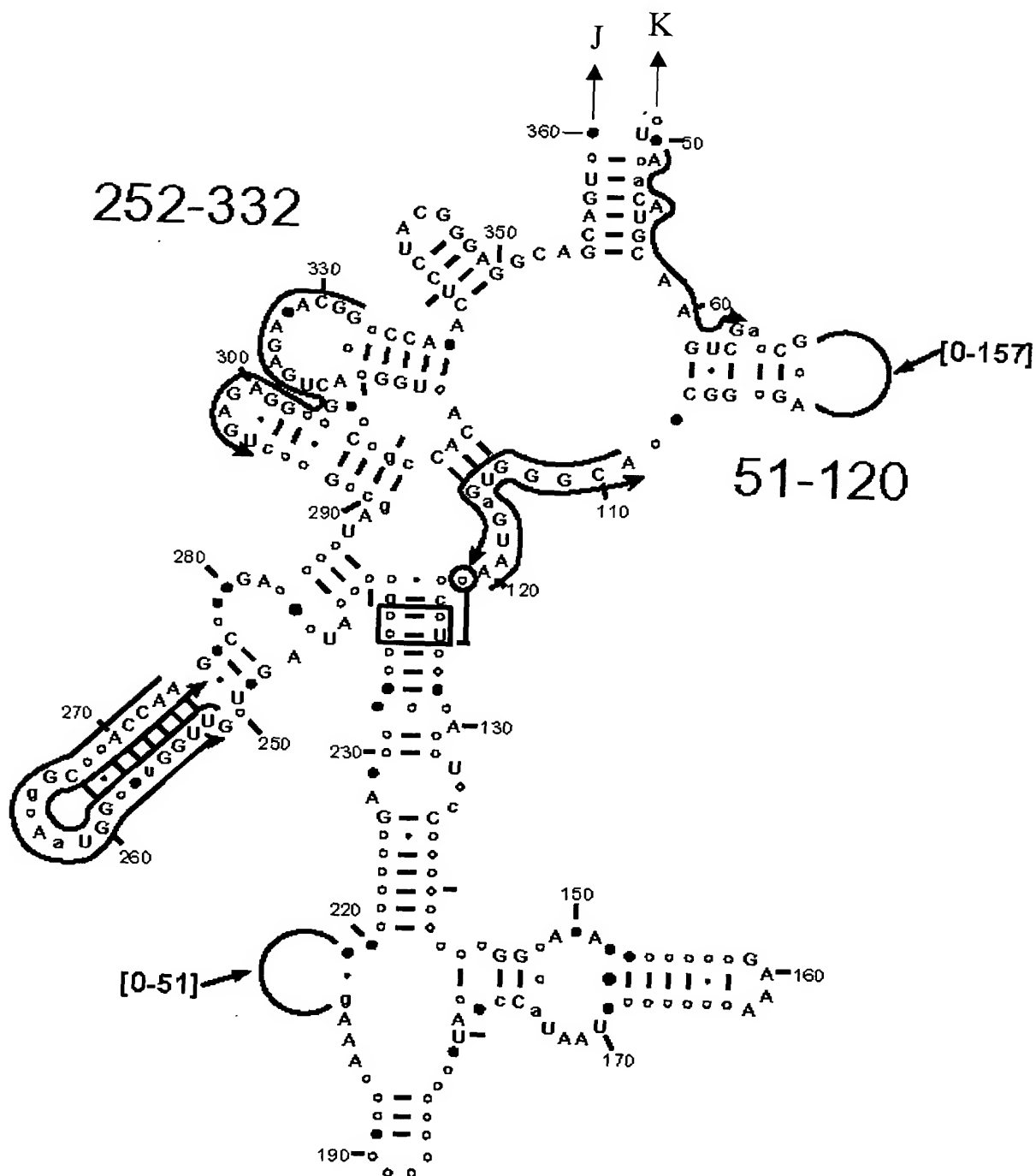


FIG. 1A-4



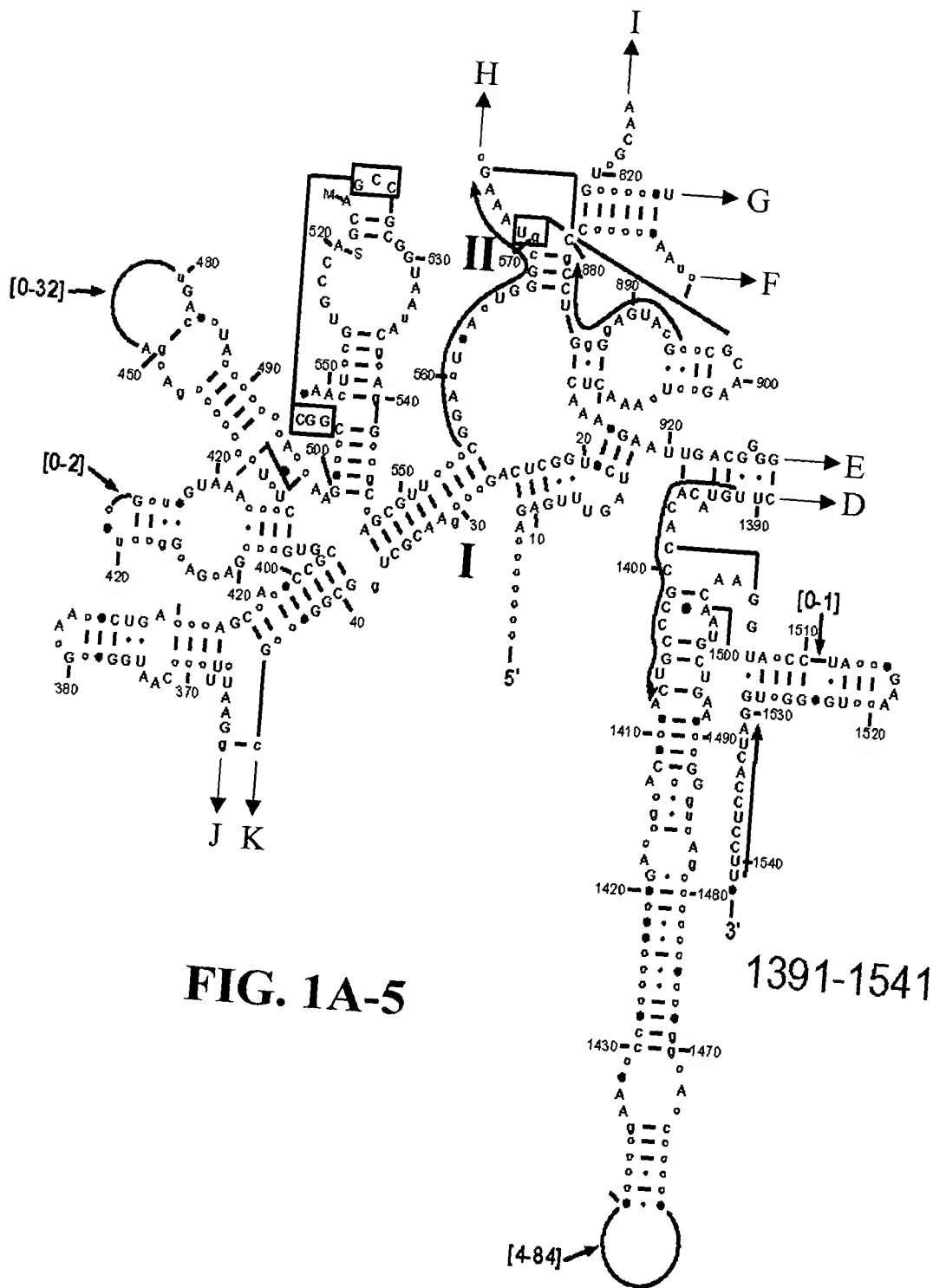


FIG. 1B

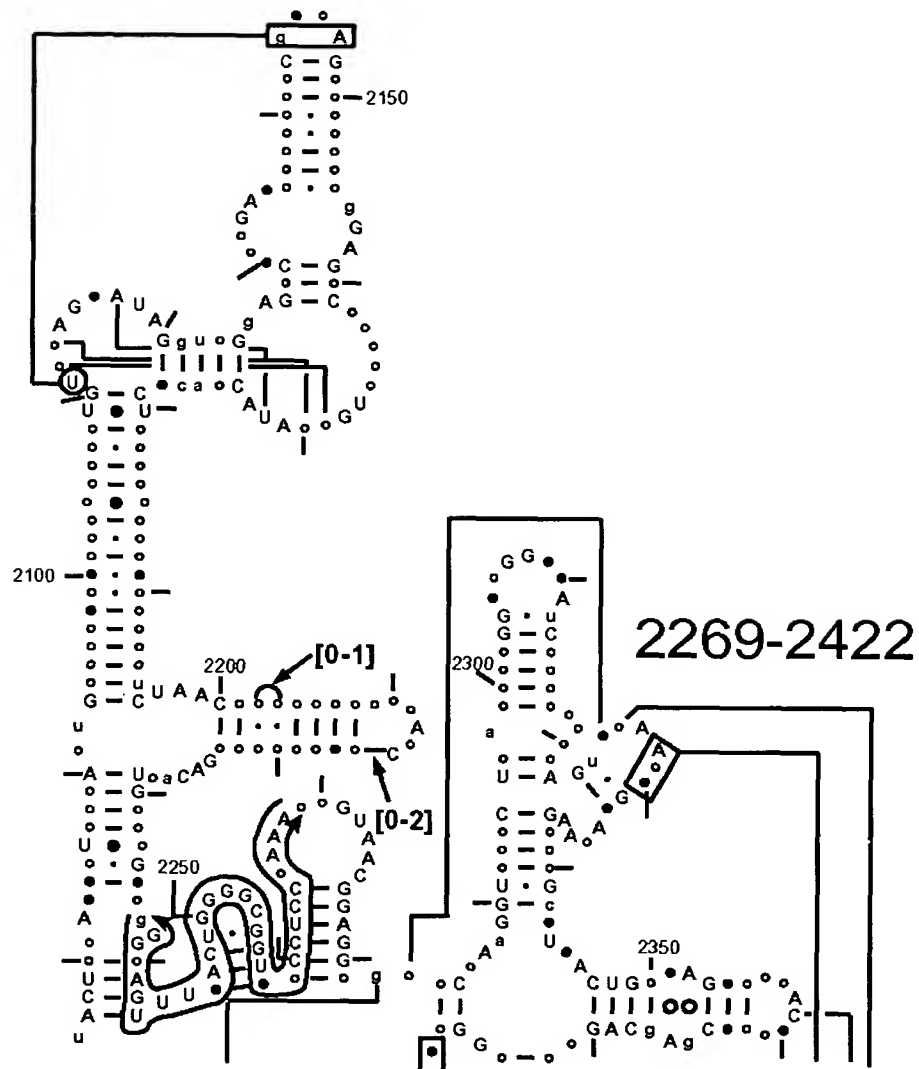
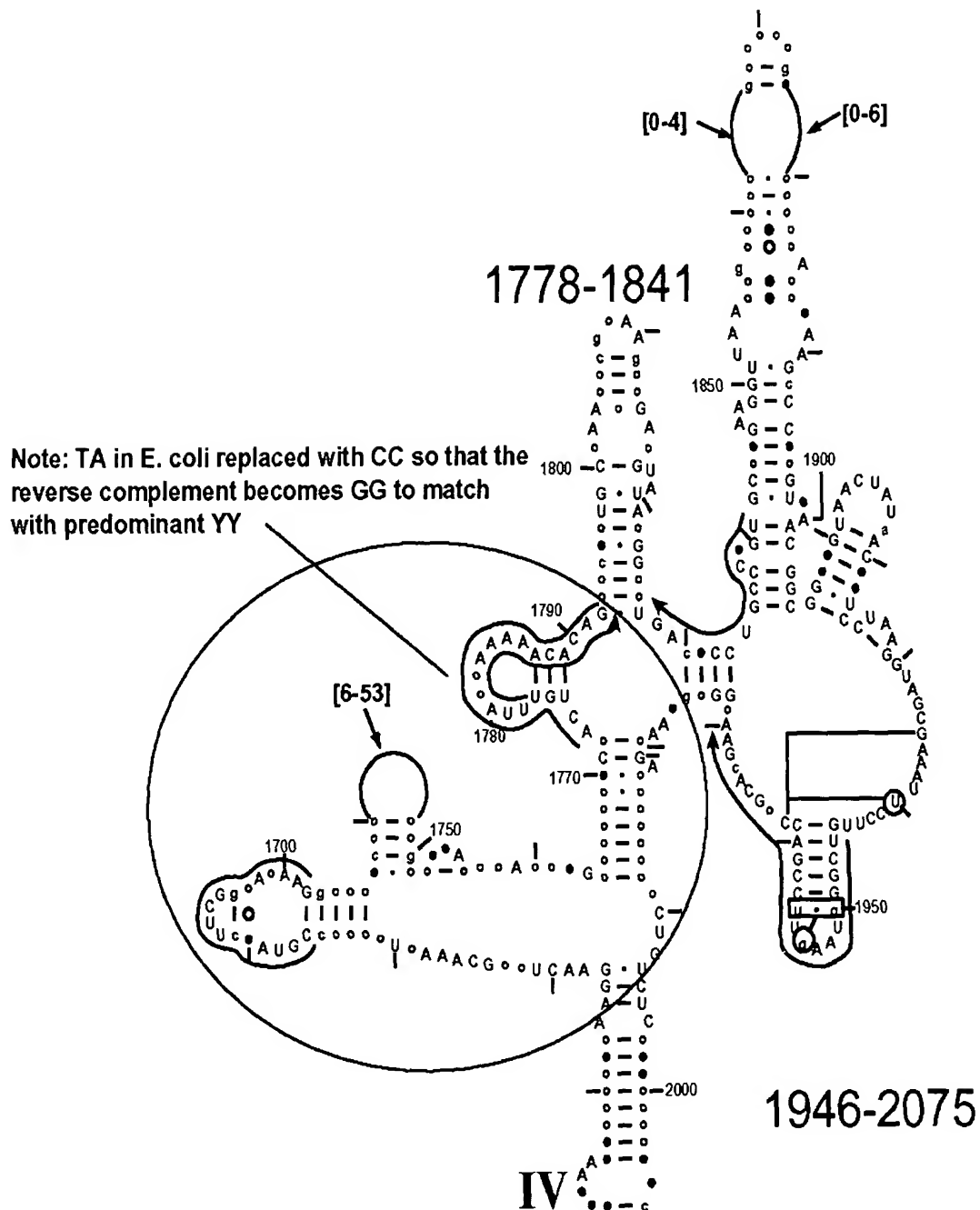
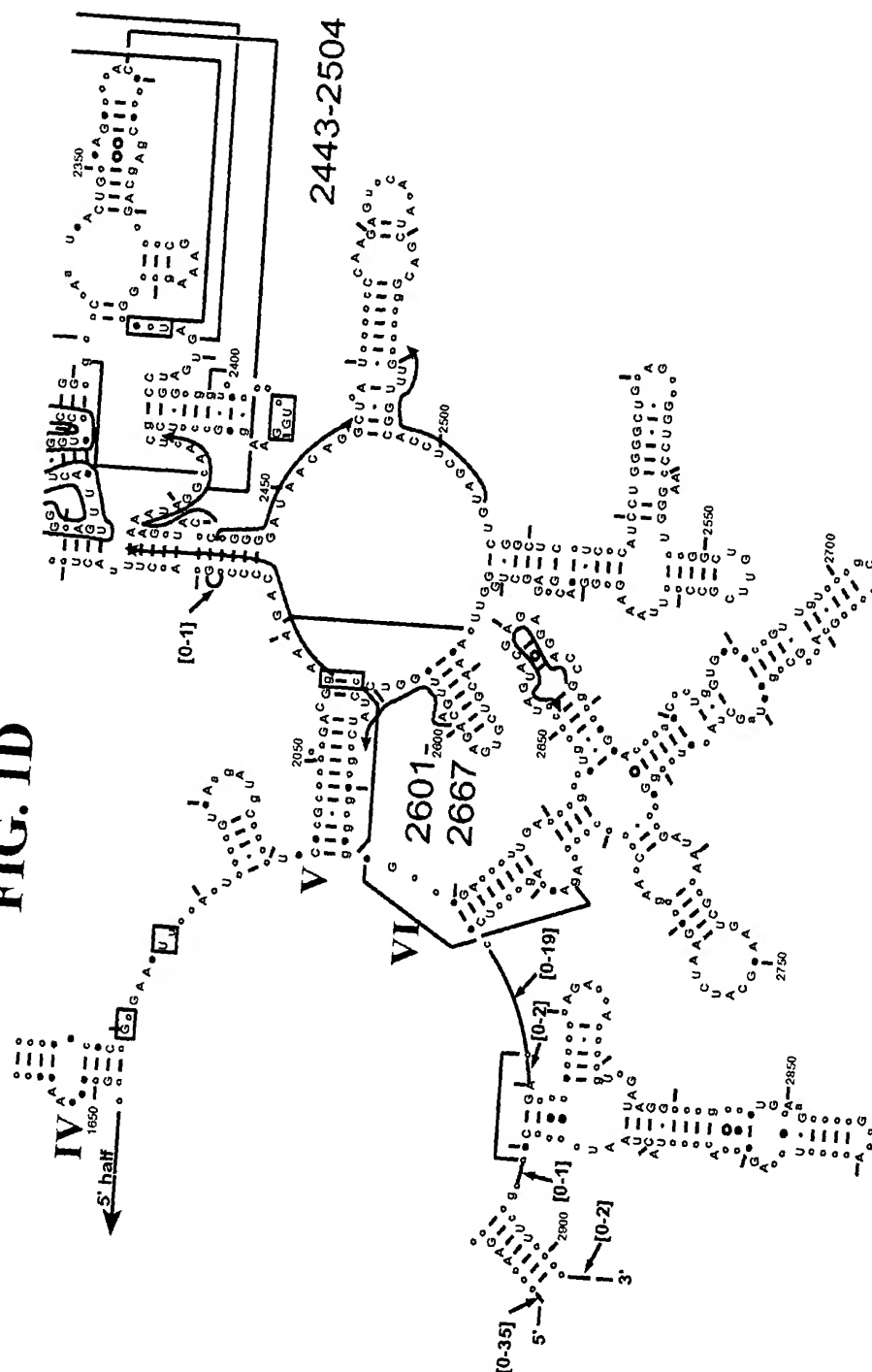


FIG. 1C





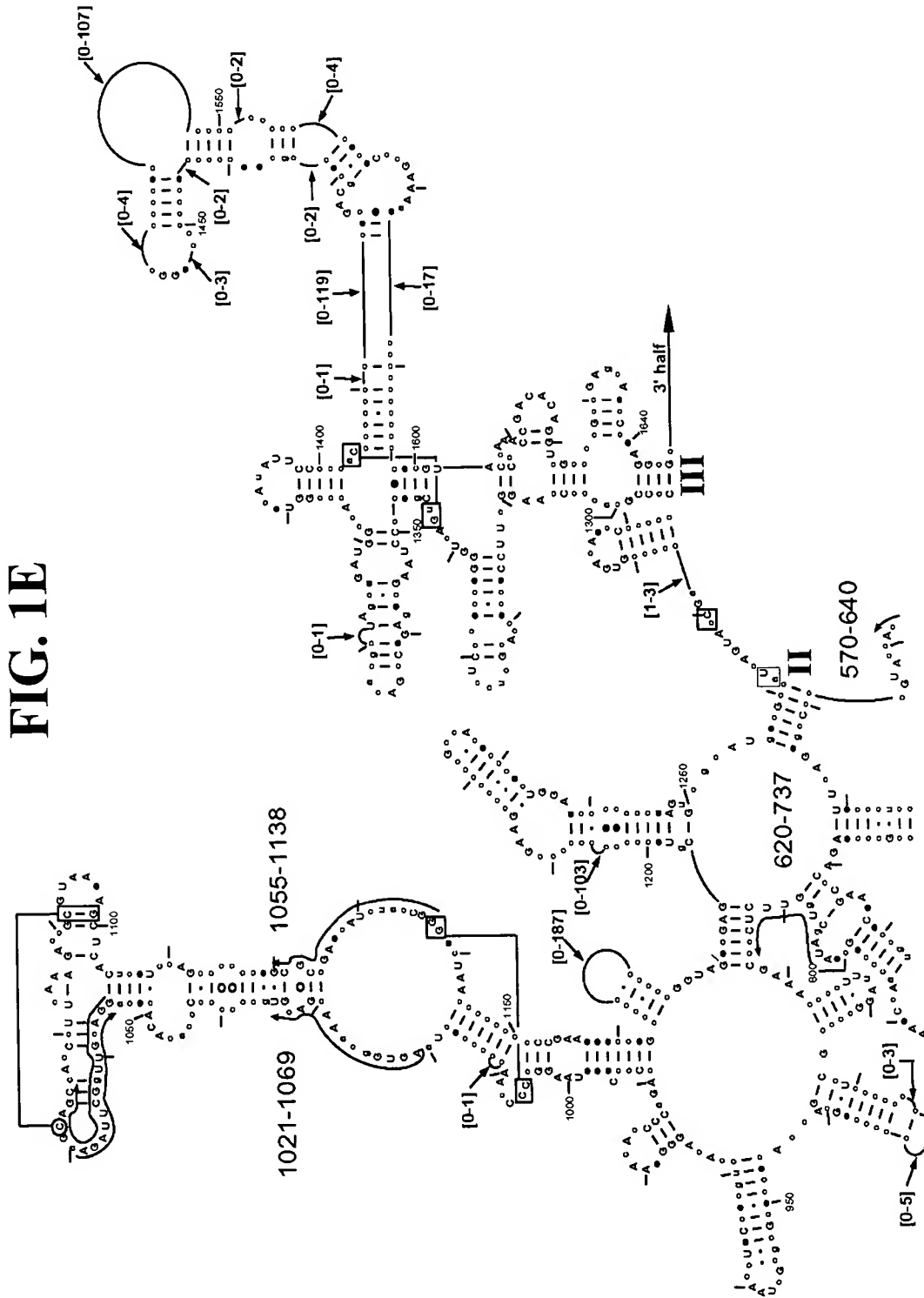


FIG. 1F

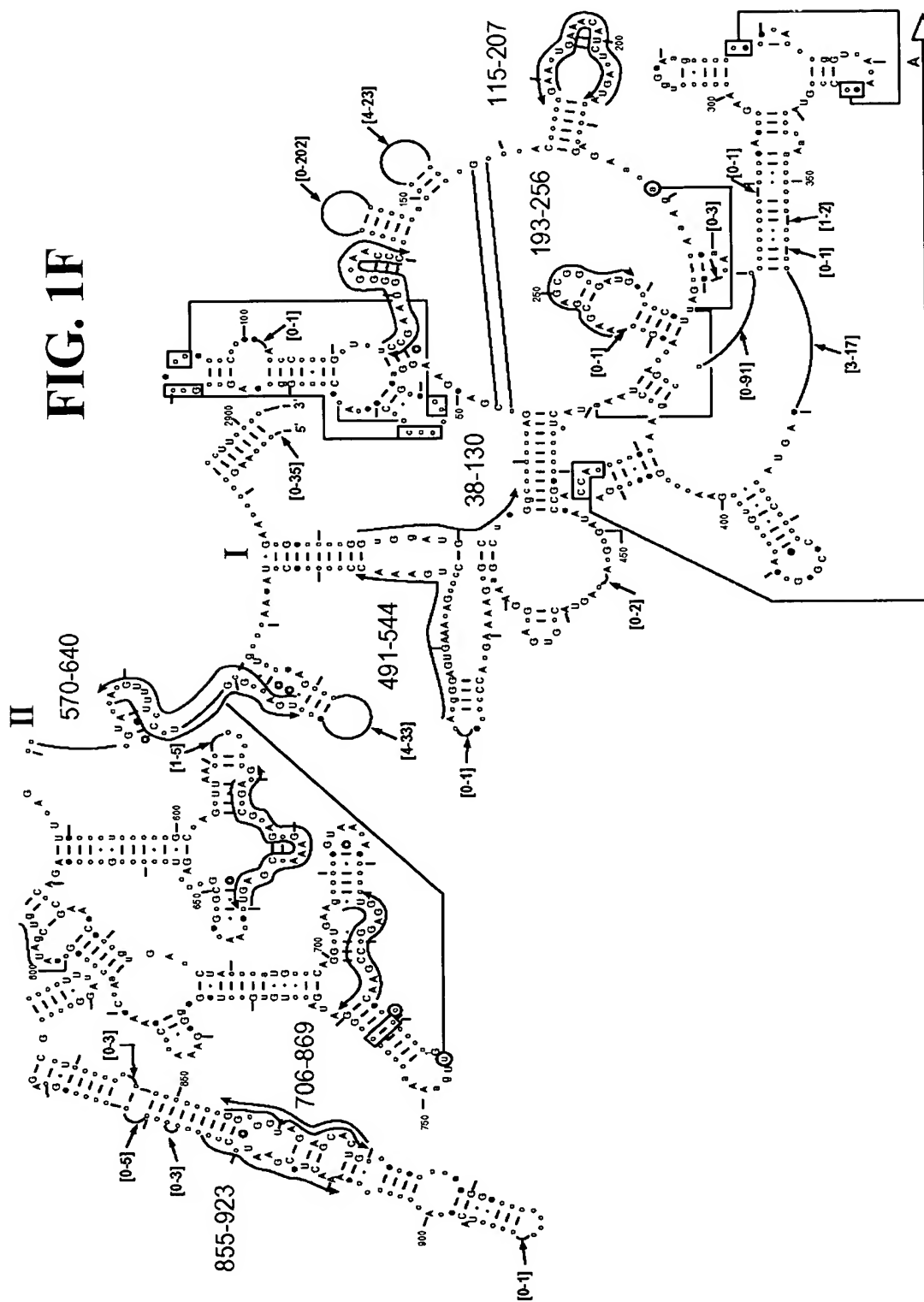


FIG. 1G

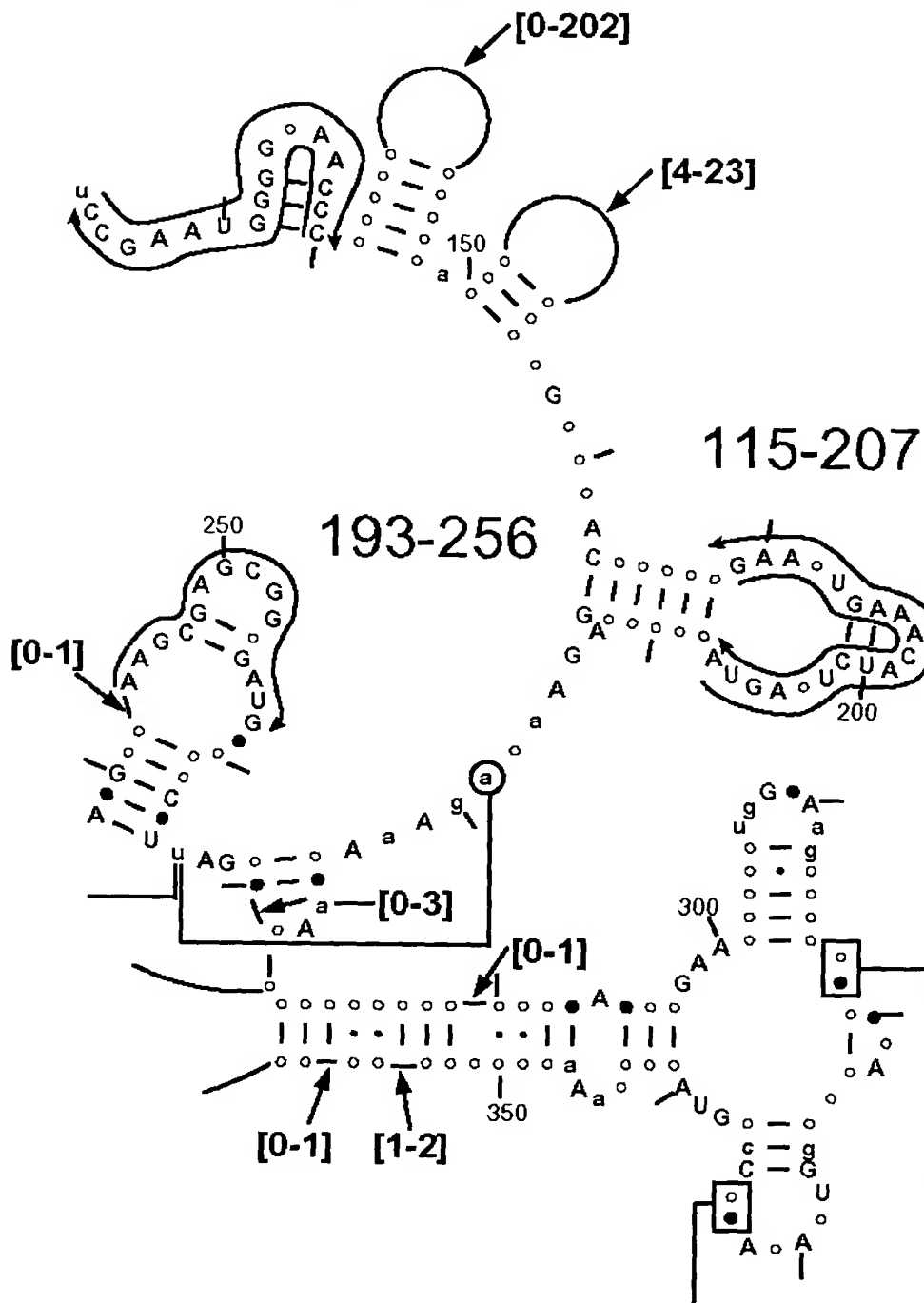


FIG. 1H

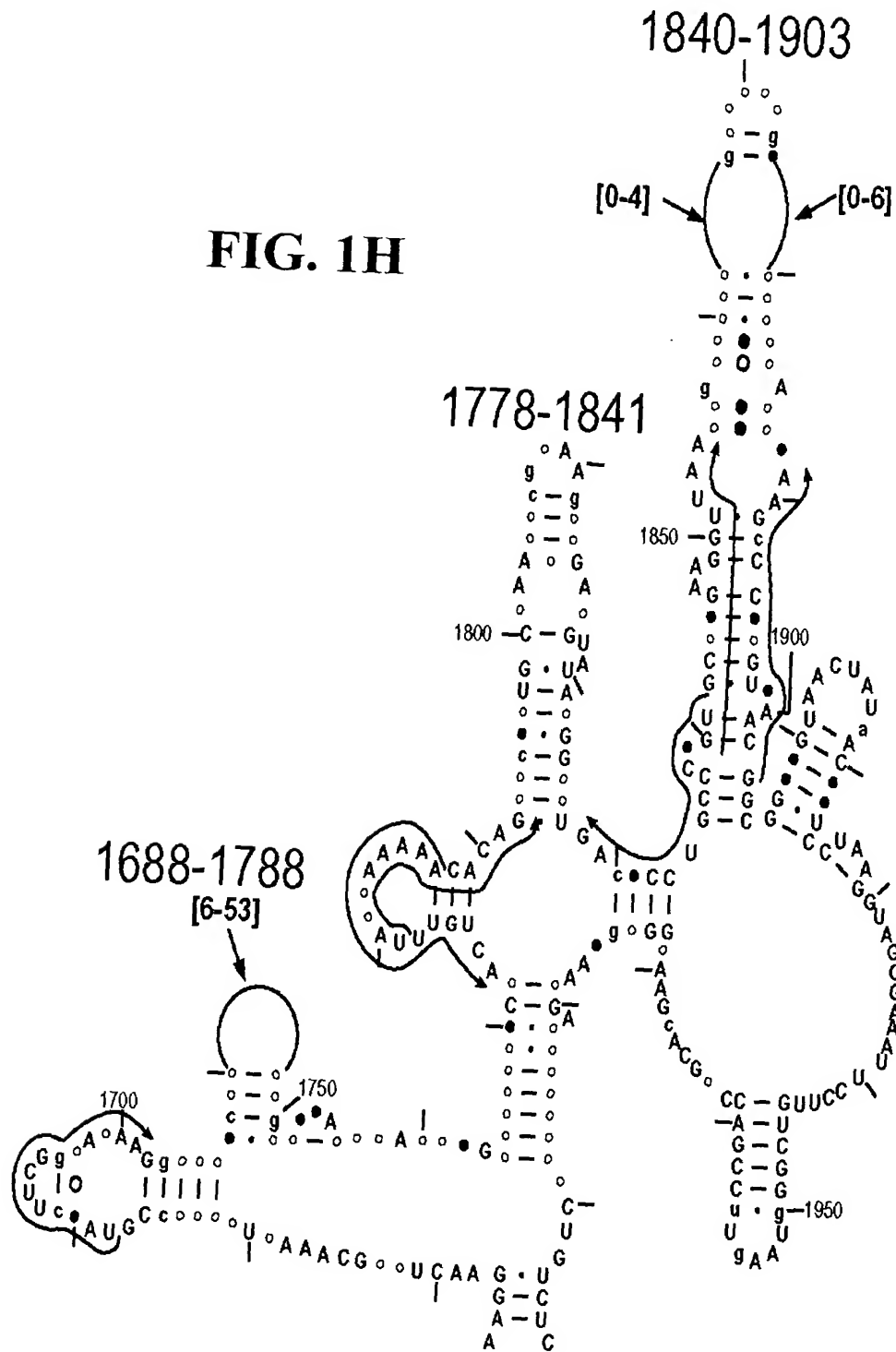


FIG. 2

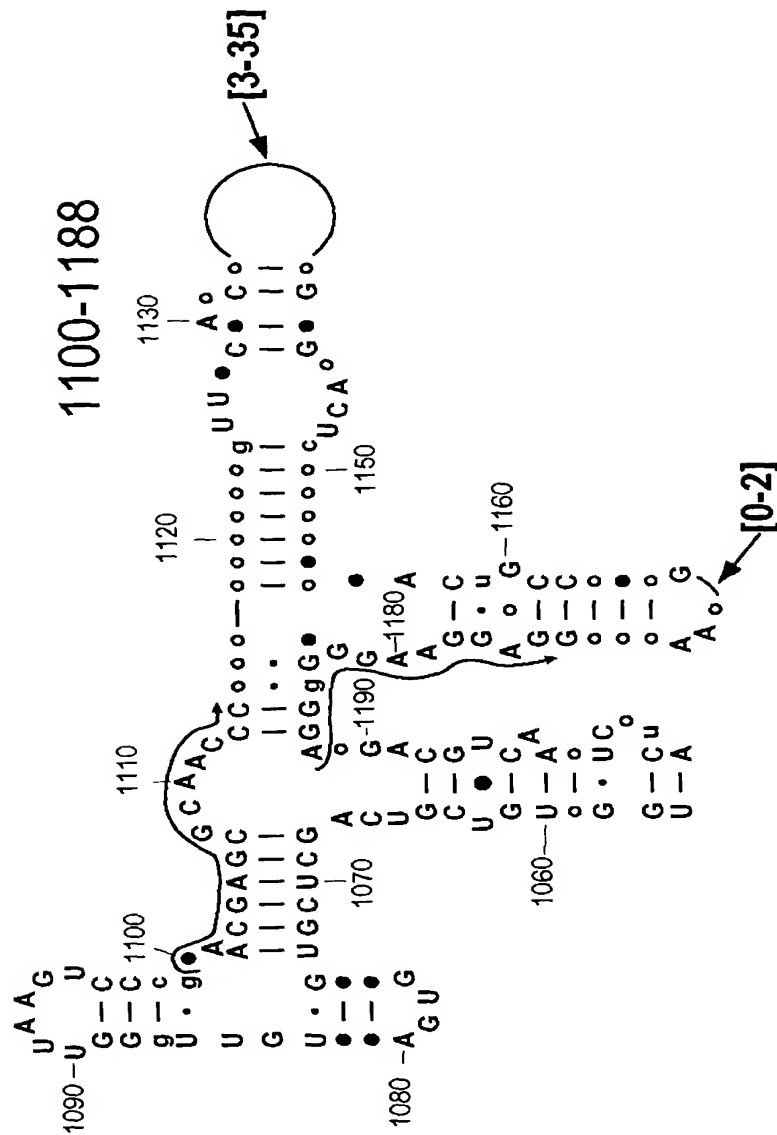


FIG. 3

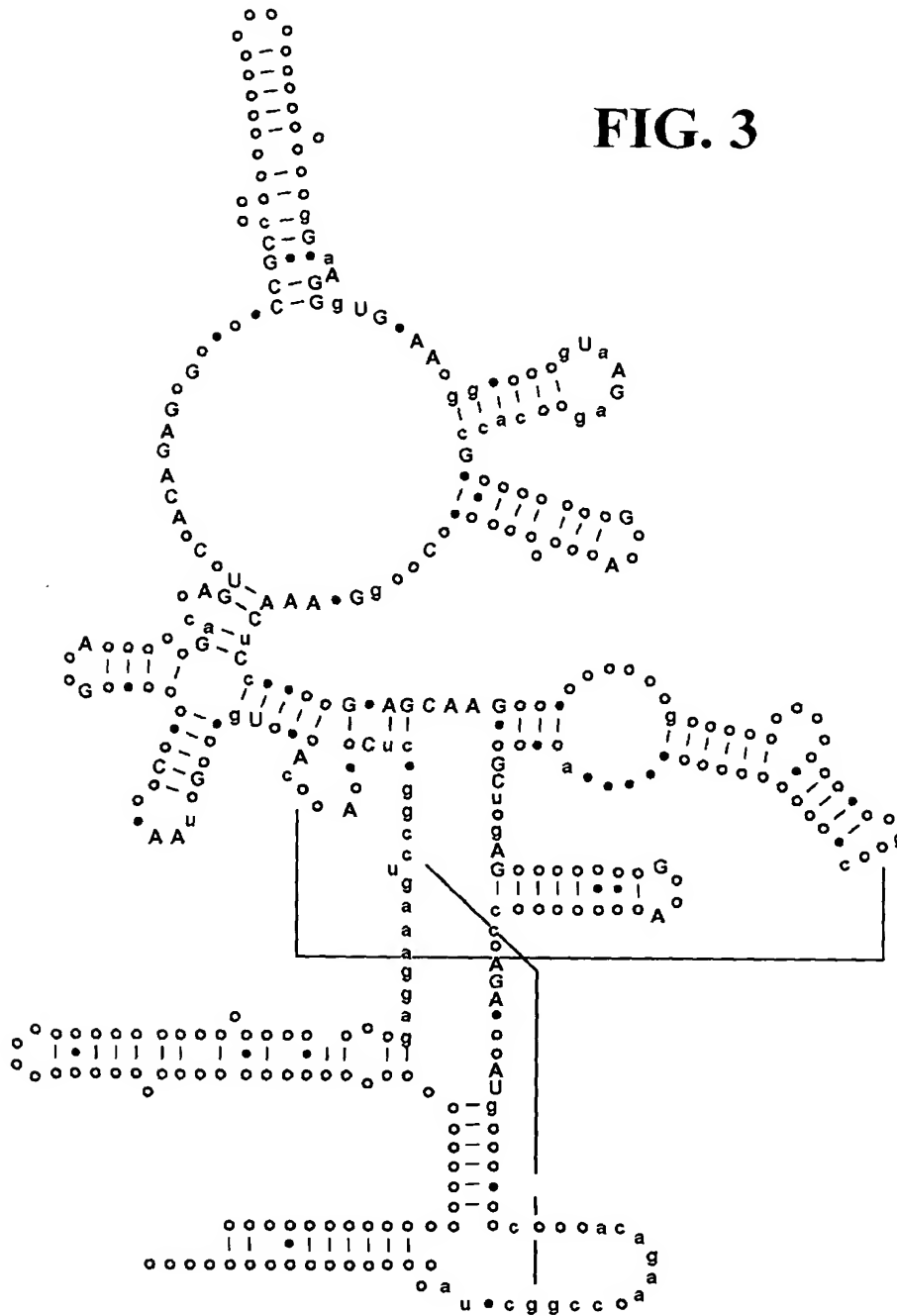


FIG. 4

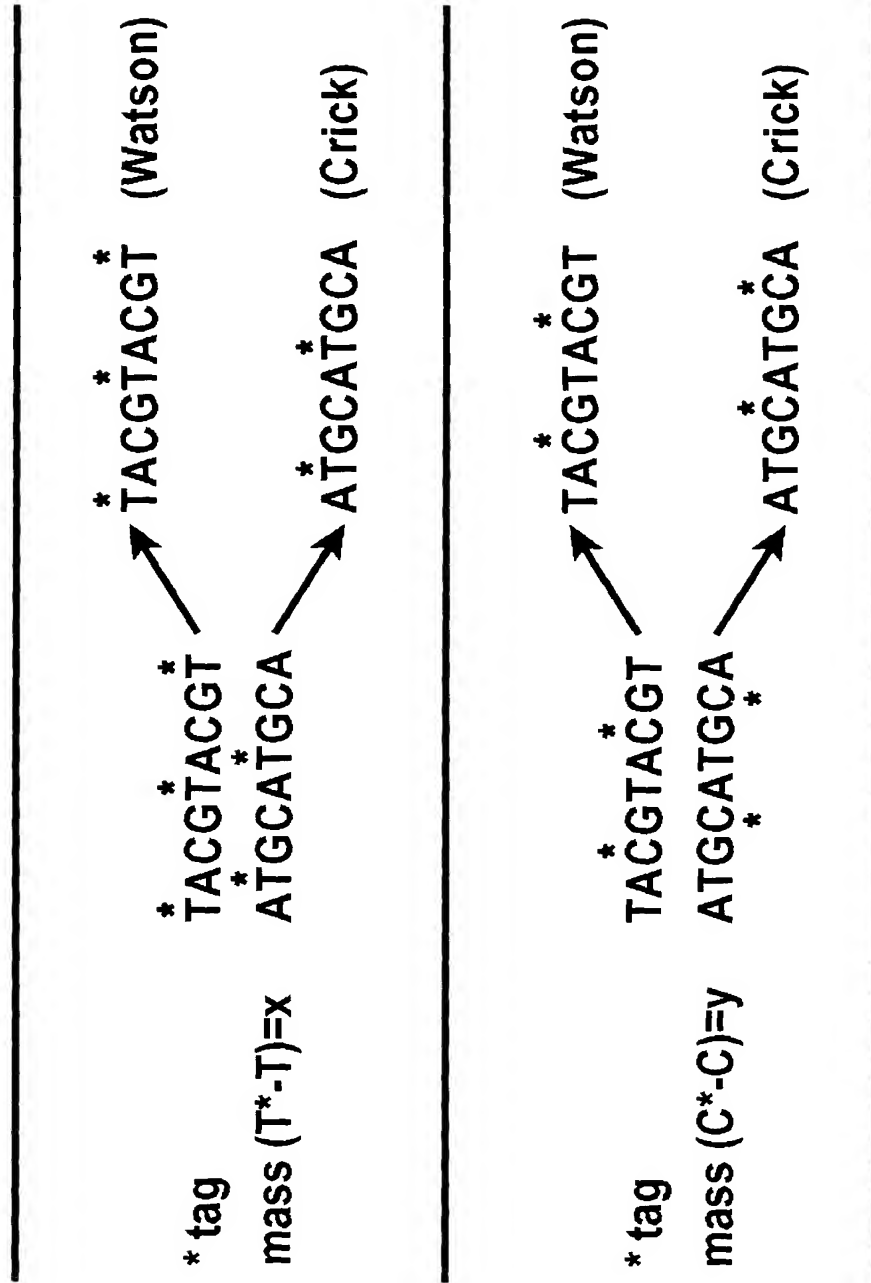
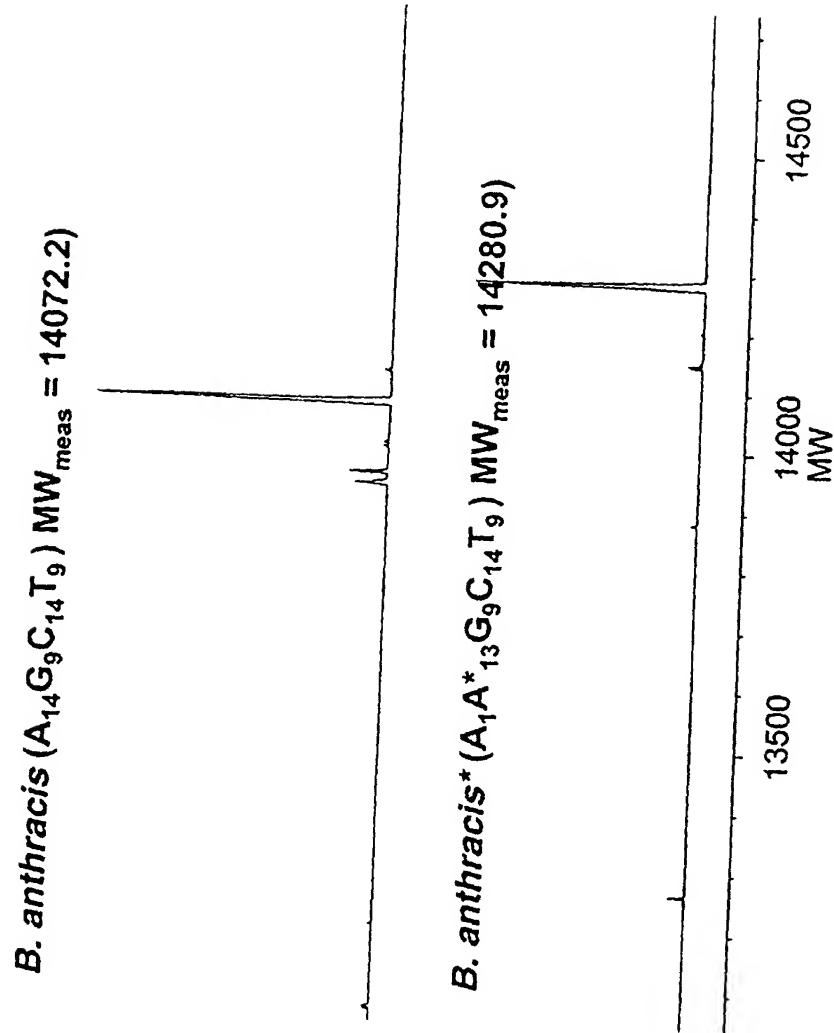


FIG. 5



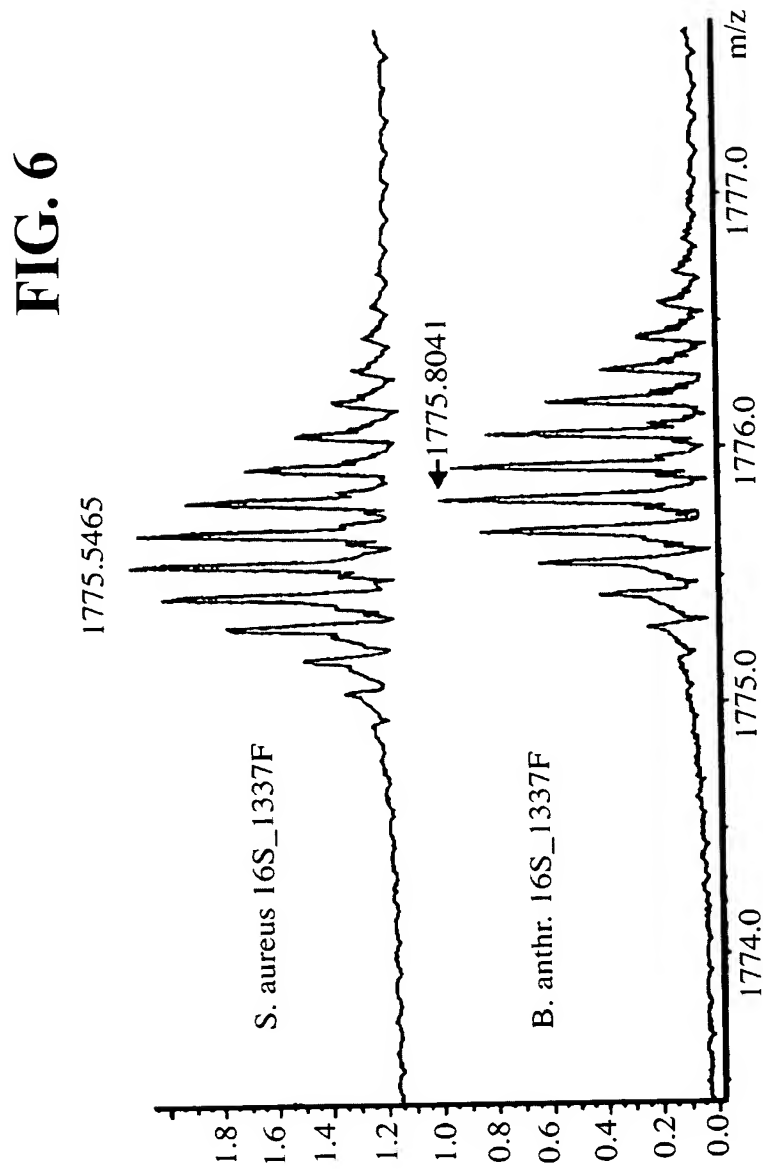


FIG. 7

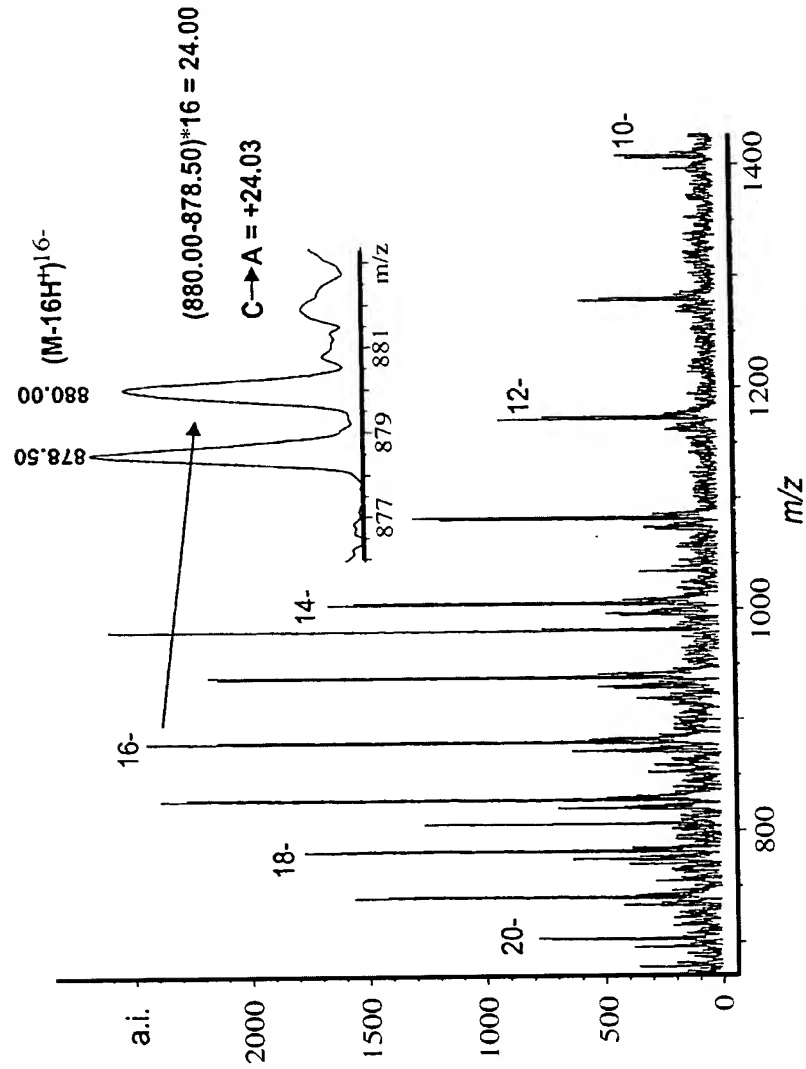
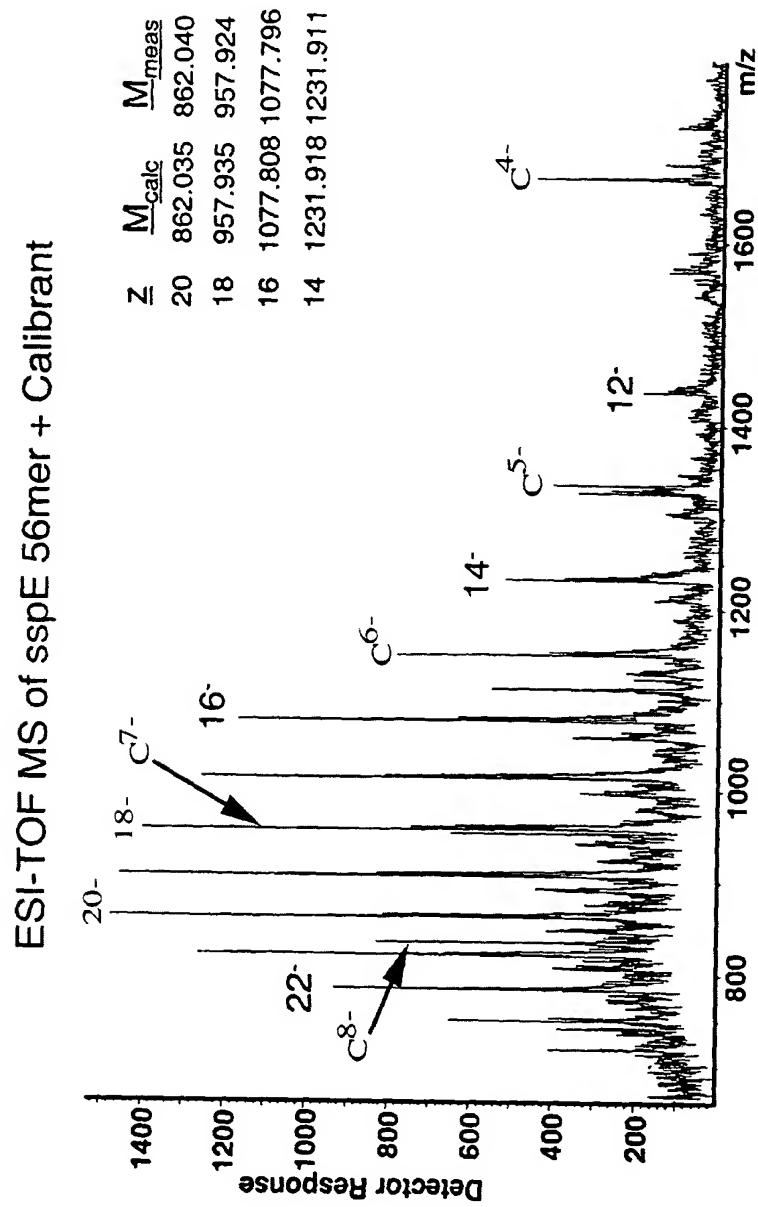


FIG. 8



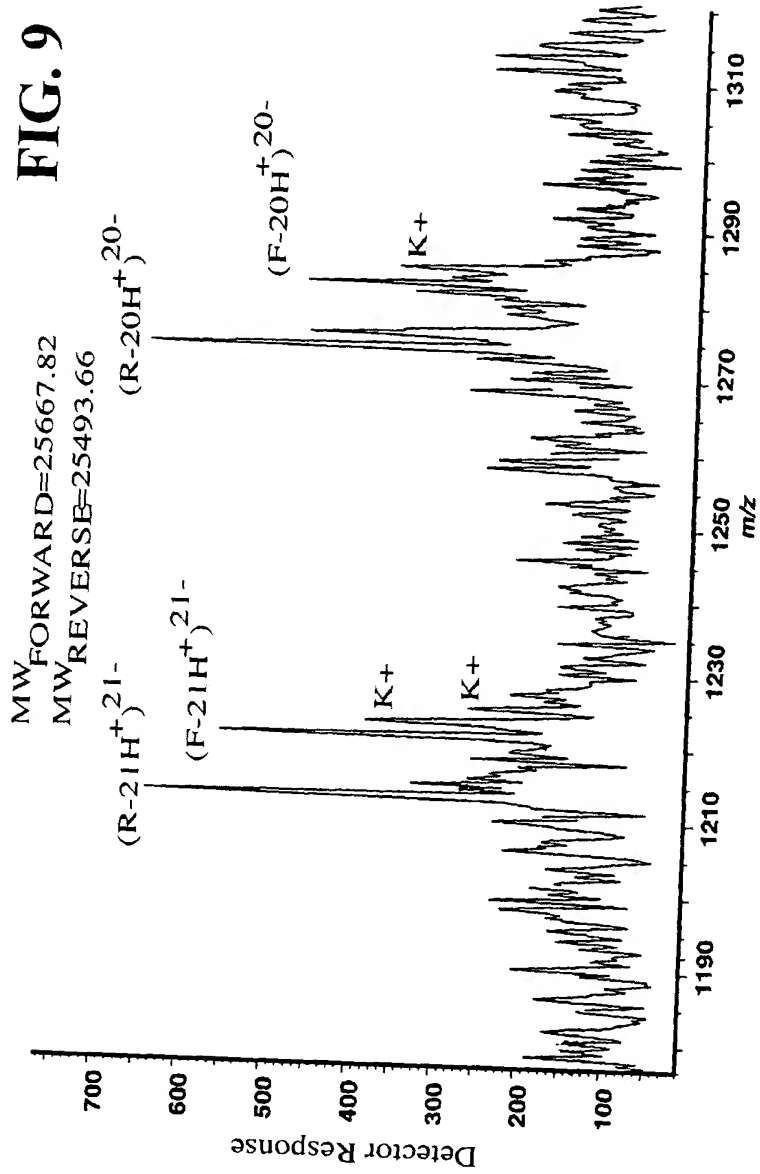


FIG. 10

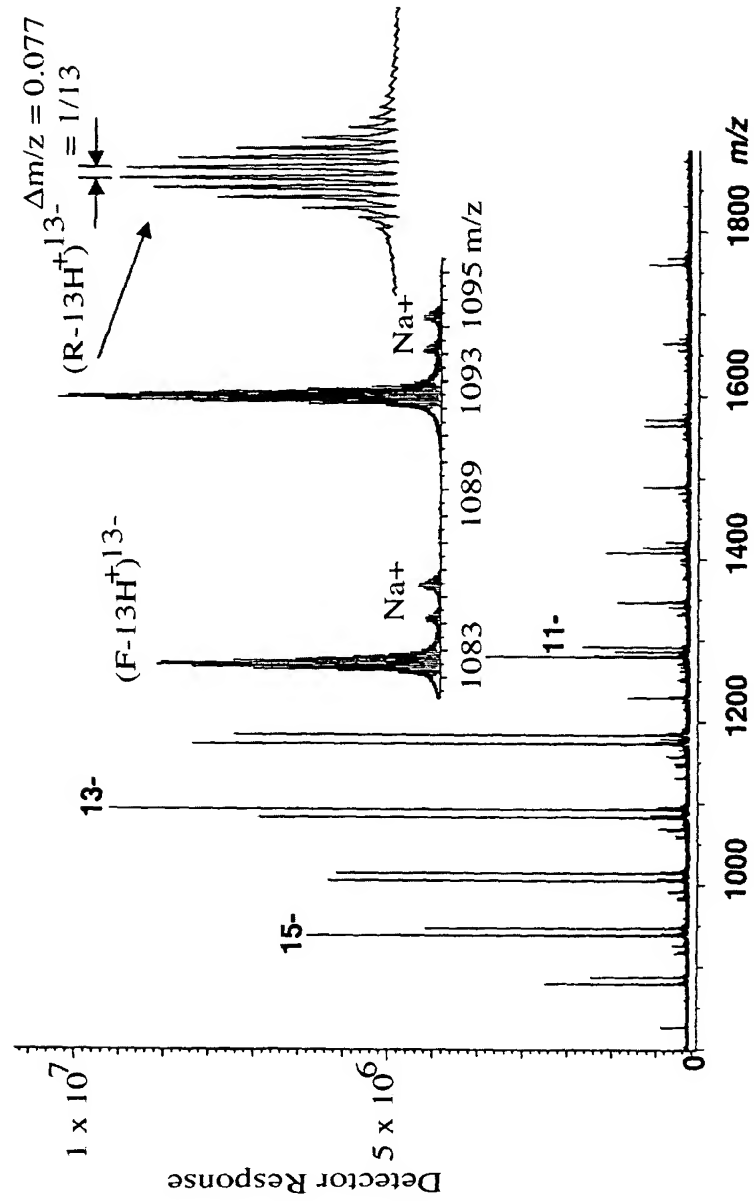


FIG. 11

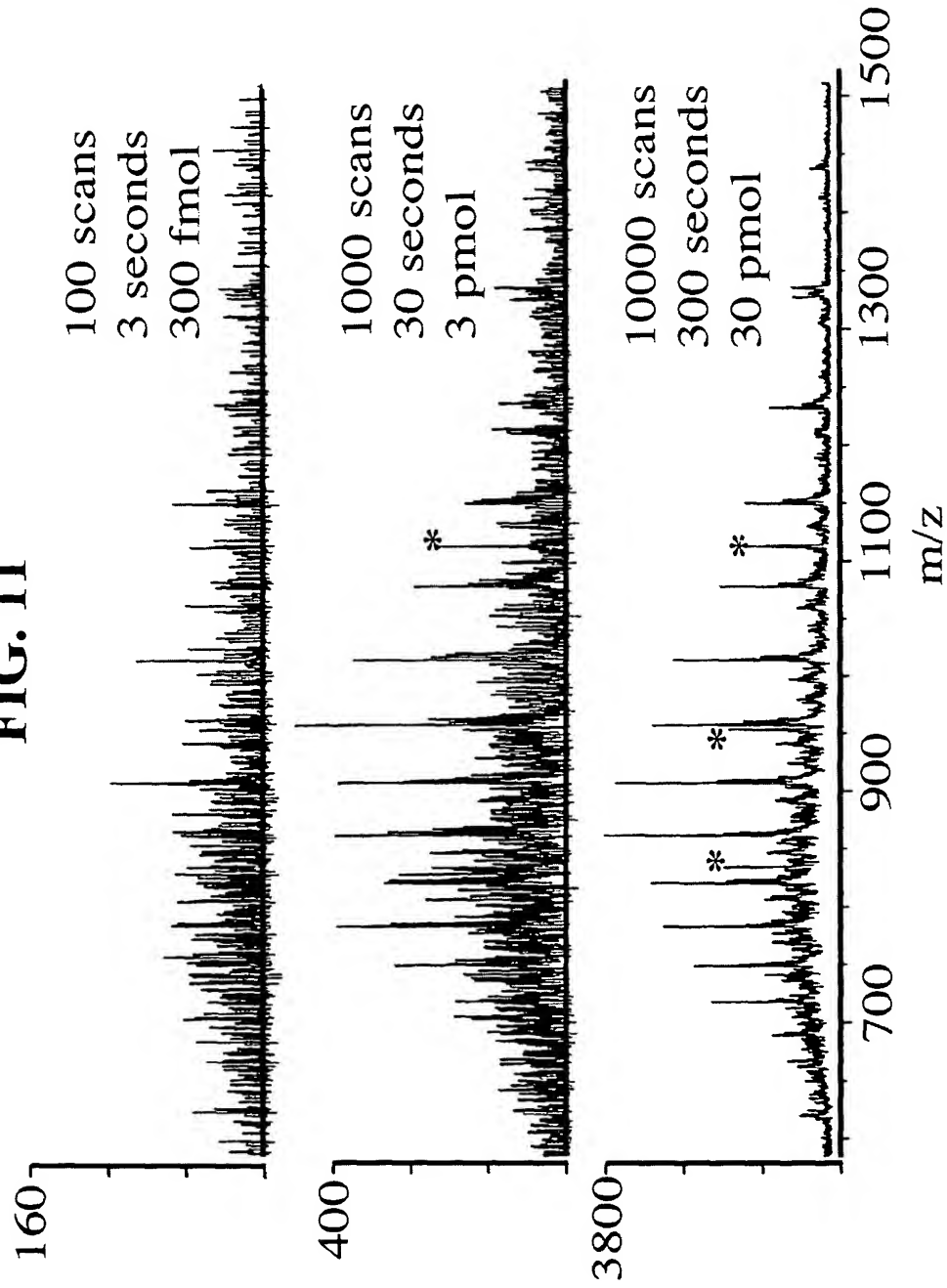


FIG. 12

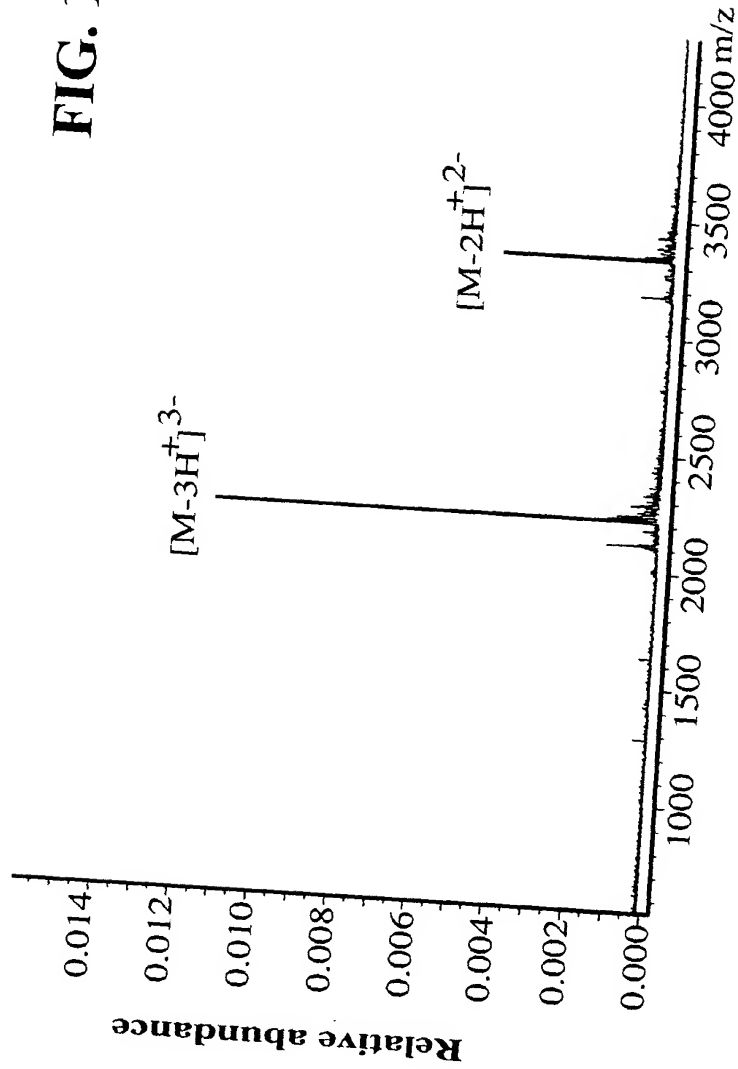


FIG. 13

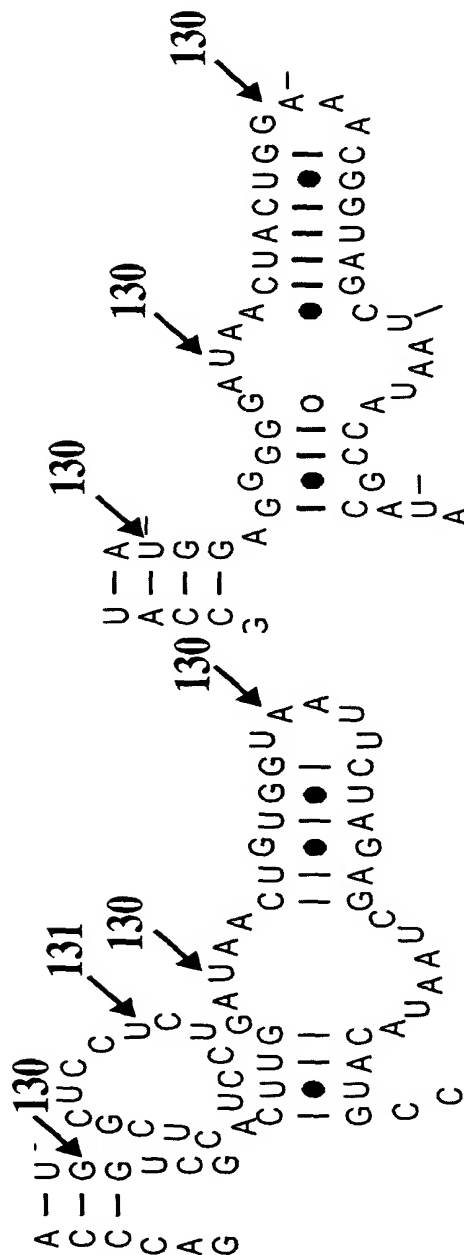
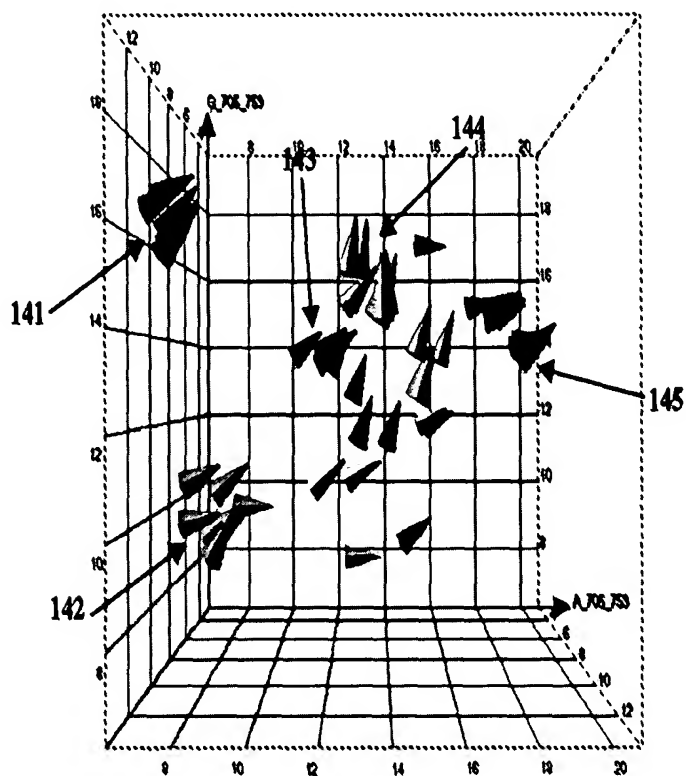


FIG. 14



Picornavirus RdRp 705-759

- | | | | |
|------------------------------|--------------------------------|-----------------------|----------------------|
| ■ Encephalomyocarditis virus | □ Foot-and-mouth disease virus | ▨ Polio | □ Rhinovirus |
| □ Enterovirus | ■ Hepatitis A virus | ■ Porcine enterovirus | ▨ Simian Hepatitis A |

FIG. 15

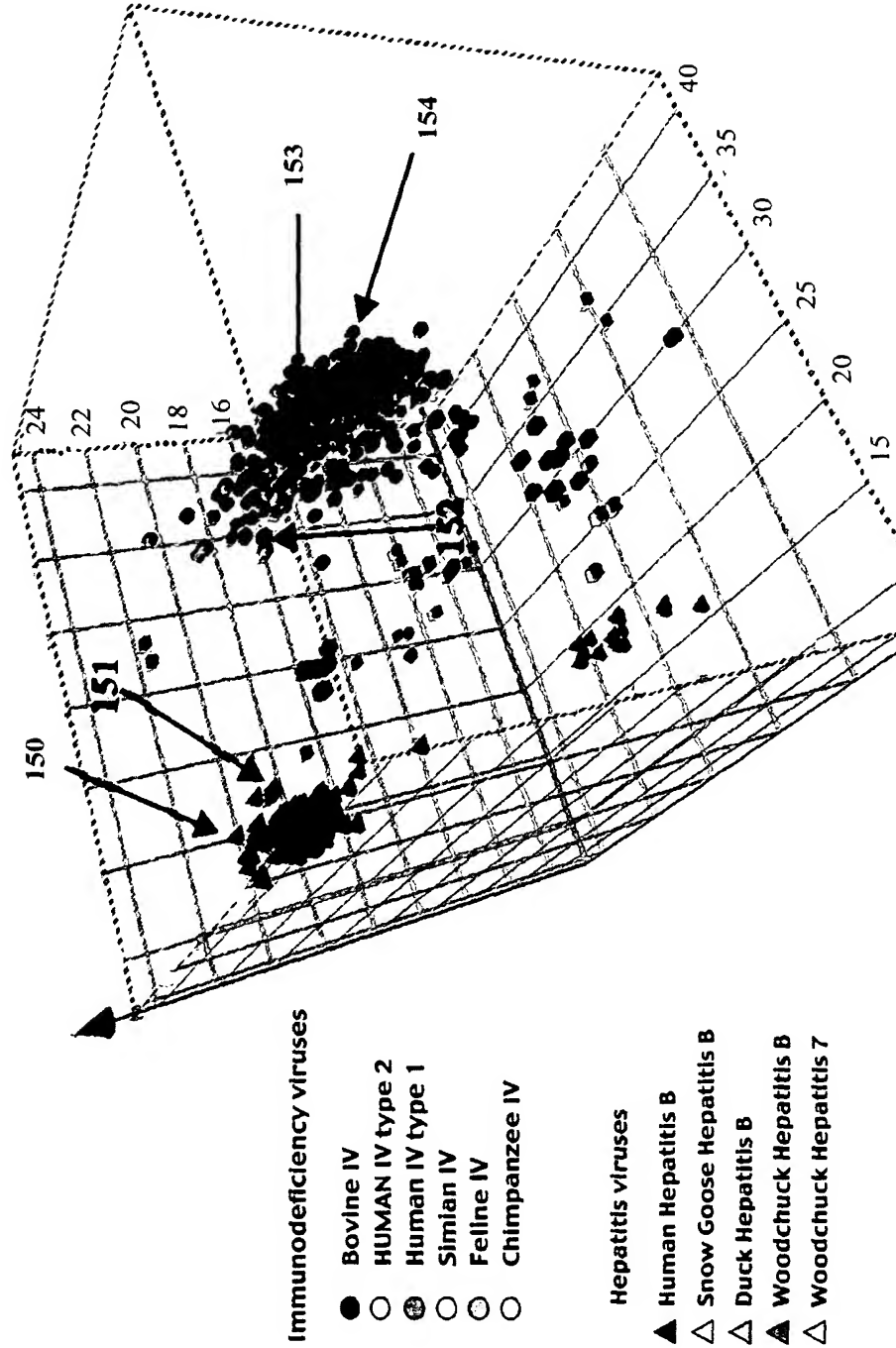
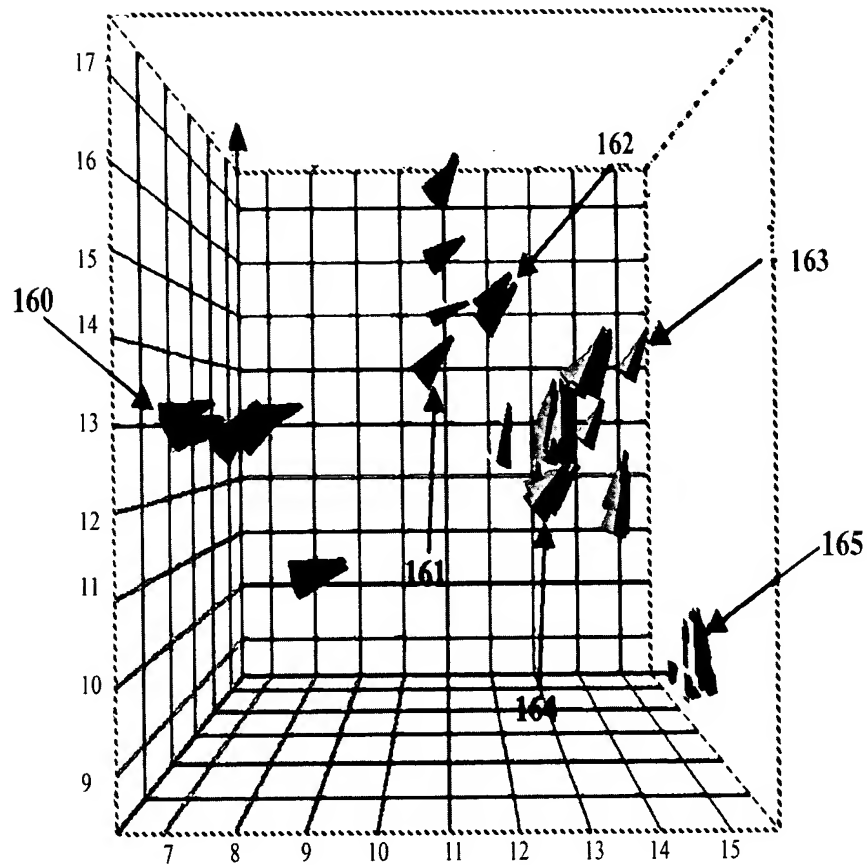
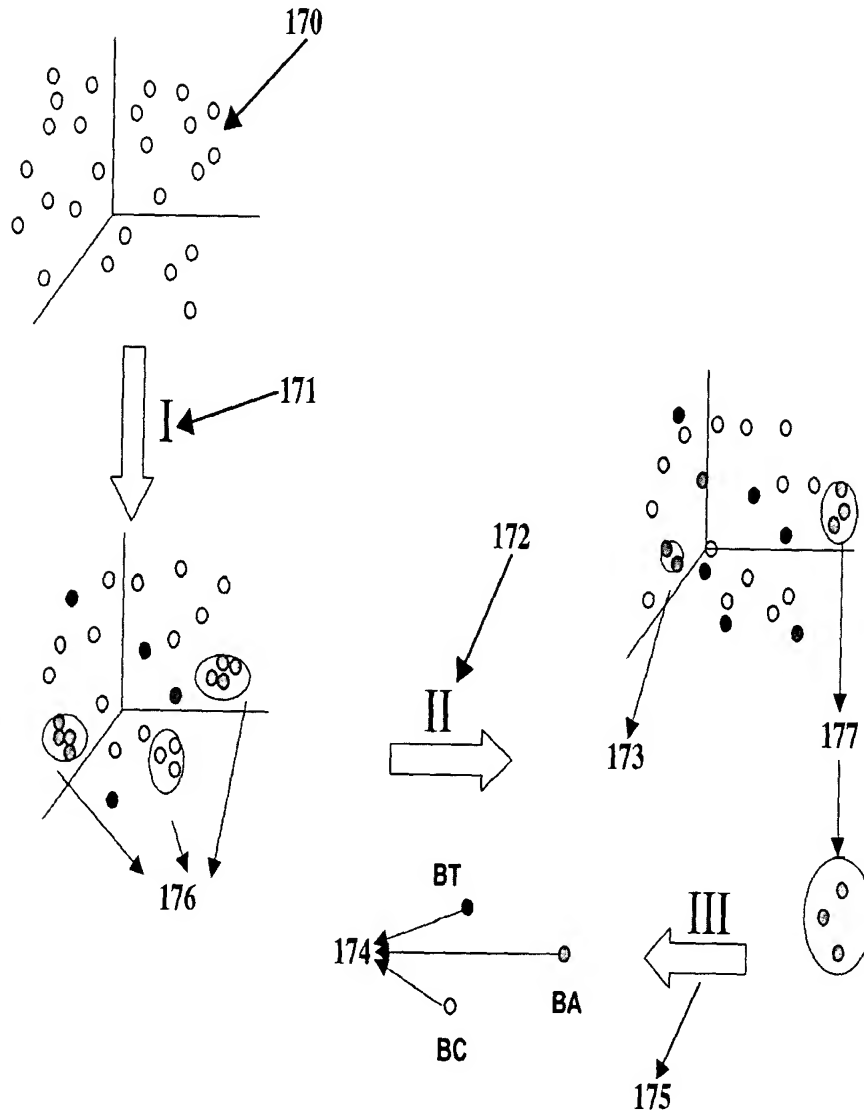


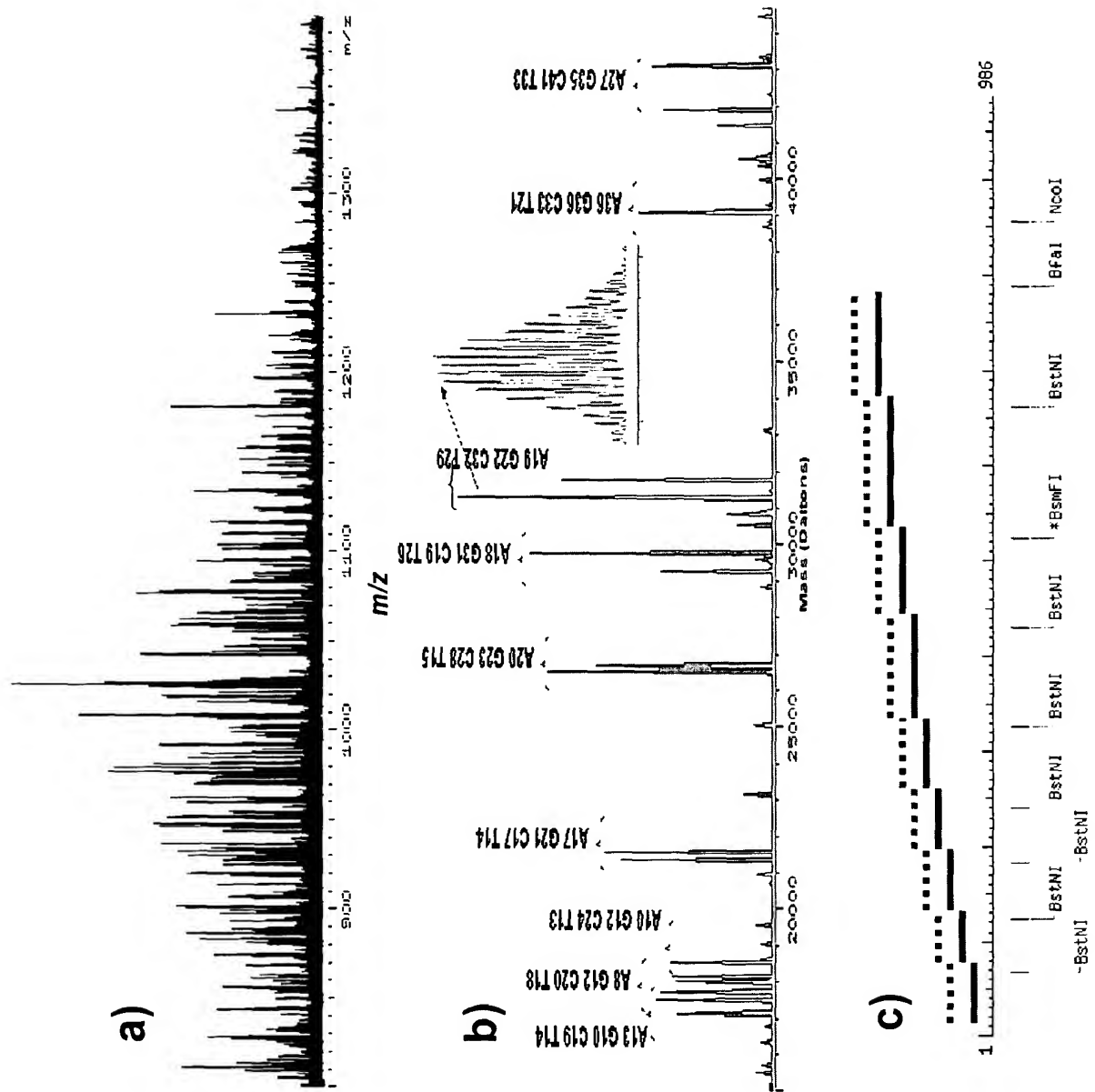
FIG. 16



- Flavi RdRp 2453-2493**
- | | | |
|-------------------|----------------------------------|-------------------------------|
| Dengue virus type | Japanese encephalitis virus | Tick-borne encephalitis virus |
| Dengue virus type | Kunjin virus | West Nile virus |
| Dengue virus type | Murray valley encephalitis virus | Yellow fever virus |

FIG. 17





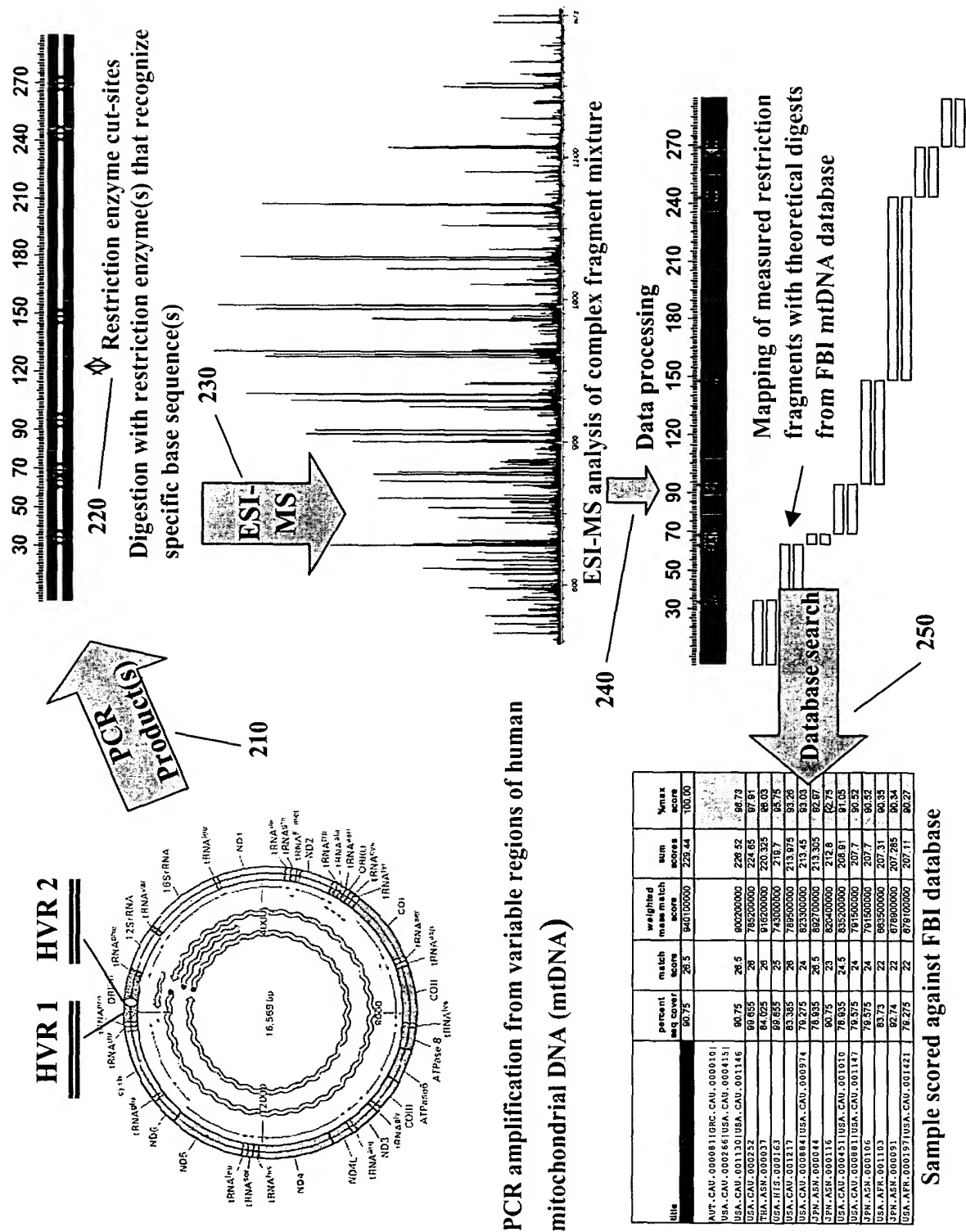
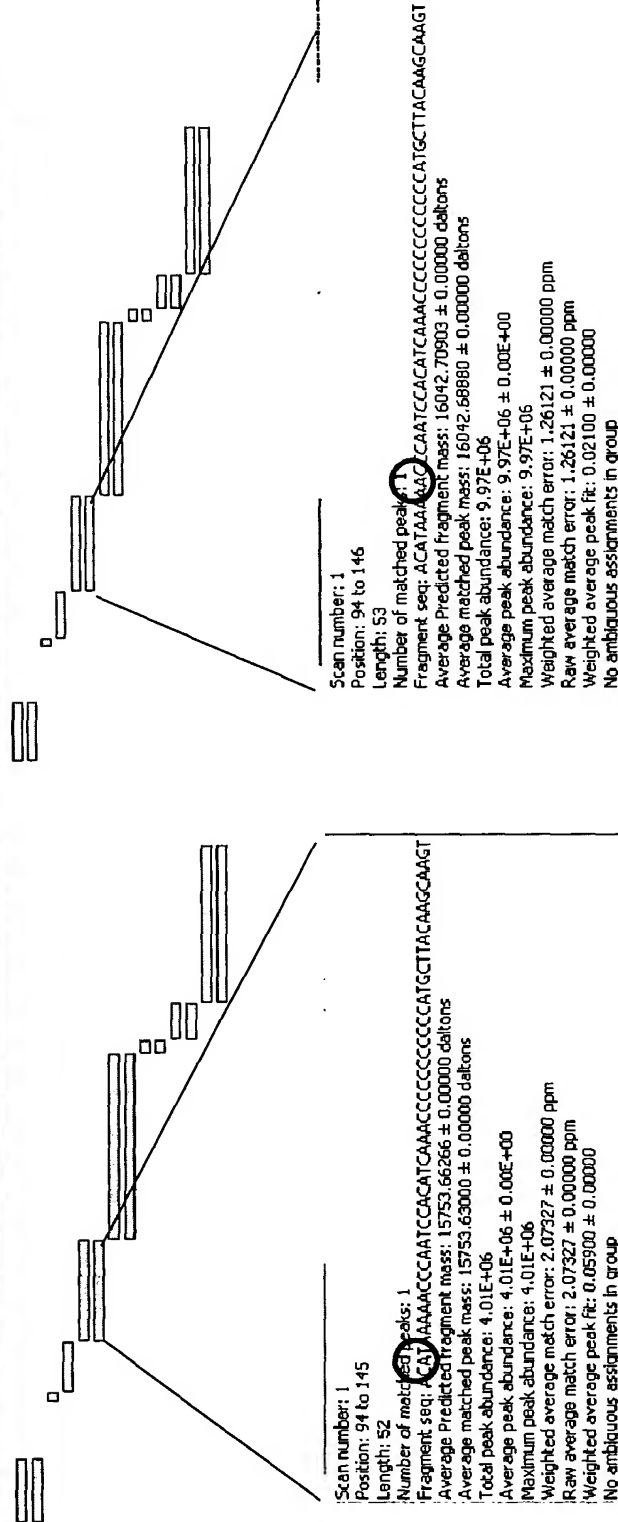


Figure 19

Sample 1: Heteroplasmy (mixture of lengths) is detrimental to sequencing approaches but does not adversely affect MS measurements

HV1-1-outer-variant1: p482_3_26_2003.pek, scan HV1-1-outer-variant2: p482_3_26_2003.pek, scan 1



(opposite strand also observed)

HV1-1-outer-variant1
HV1-1-outer-variant2

(opposite strand also observed)

acataaaaaaaccaatccacatcaaaacccccccccccatgcttacaagcaag
acataaaaaaaccaatccacatcaaaacccccccccccatgcttacaagcaag

Heteroplasmic region

Figure 20A

Figure 20B

MS Approach Succeeds Where Conventional Sequencing Fails

Sequences differ in length by one base in the 'C' stretch. Both variants appear in digest data. Sequencing profile also points to a length variation in this region: Example trace: 040803_81_A1_HV1-1_1560F_A11.AB1

